

I

CC CKR2B	MLSTSRSRFIRNT	NEEGEV--TTFFDYDY--GAPCHREFDVKQIGAQLLPPLYSVTFIFGVGNMLVVLILINCKKLKCLTDIYLLNLAI	SDLLPLITLPLMAH-8AANEWVT
CC CKR5		HDYQV-SSPIYDINYYTSEPCQKINVKQLAARLLPPLYSVTFIFGVGNMLVVLILINCKKLKCLTDIYLLNLAI	SDLLPLITLPLMAH-8AANEWVT
CC CKR1		METHNTJEDYDTT-----EFDYGDATPCQKVNREAFGAQLLPPLYSVTFIFGVGNMLVVLILINCKKLKCLTDIYLLNLAI	SDLLPLITLPLMAH-8AANEWVT

100	120	140	160	180	200	220
GNAMCKLPTGLYHIGYFGGIPFIILLTIDRYLAIVHAVTALKARTVTFGVWTSVITWLVAVTASVPGIIFTRKOKEDSVVCGPYPPRG---- <td>LLIMVTCYSGILKTLRCR</td> <td></td> <td></td> <td></td> <td></td> <td></td>	LLIMVTCYSGILKTLRCR					
GNTHCQLLTGLYFIFGPFSGIFFIILLTIDRYLAIVHAVTALKARTVTFGVWTSVITWLVAVTASVPGIIFTRKOKEDSVVCGPYPPRG---- <td>LLIMVTCYSGILKTLRCR</td> <td></td> <td></td> <td></td> <td></td> <td></td>	LLIMVTCYSGILKTLRCR					
GDAMCKILSGFYTGLYSEITFIILLTIDRYLAIVHAVTALKARTVTFGVWTSVITWLVAVTASVPGIIFTRKOKEDSVVCGPYPPRG---- <td>LLIMVTCYSGILKTLRCR</td> <td></td> <td></td> <td></td> <td></td> <td></td>	LLIMVTCYSGILKTLRCR					

100	120	140	160	180	200	220
NEKKRHRVAVRVIITINIVYTLFWTPYINIVILLNTFOHFFGLSNCESTSQLDQATQVTETLGHTHCCINPIIYAFVGEKFRYLSVTFPRKBITKRFCKQC	PVTFYRETVDGVTSTNTPSTGCEQVSAAGL					
NEKKRHRVAVRVIITINIVYTLFWTPYINIVILLNTFOHFFGLSNCESTSQLDQATQVTETLGHTHCCINPIIYAFVGEKFRYLSVTFPRKBITKRFCKQC	PVTFYRETVDGVTSTNTPSTGCEQVSAAGL					
NEKKS-KAVRLIFVIMIIIFLFWTPYNLTILISVTFQDPLFTHZCEQSRHLDLAVQVTEVIAVTHCCVNEPVIYAFVGERPDKYLRLQPLFRRVAVHLVKWL	PPLSVDRRLERVSSTSP-STGEHEL	SAGF				

FIGURE 1A

```

1      31      11
GAT CCG TCG ACC GCG ATT ATG GAT GGA TCG CAA GAA ACT CTC GCG CCG TCG AAC AAG(ATT)
asp pro ser thr ala ile met asp gly trp gln glu thr leu pro gly trp asn lys met
61 / 21      91 / 31
GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA TCG GAG CCG TCG CAA
asp tyr gln val ser cor pro ile tyr asp ile asn tyr tyr thr ser glu pro cys gln
121 / 41      151 / 51
AAA ATC AAT GTG AAG CAA ATC GGA GAG CCG CTC CTG CCT CCG CTC TAC TCA CTG CTG TTC
lys ile asn val lys gln ile ala ala arg leu leu pro pro leu tyr cor leu val phe
181 / 61      211 / 71
ATC TTT GGT TTT GTG GGC AAG ATG CTC CTC ATC CTC ATC CTC ATA AAC TCG AAA AGG CTC
ile phe gly phe val gly asn met leu val ile leu ile leu ile asn cys lys arg leu
241 / 81      271 / 91
AAG AGC ATG ACT GAC ATC TAC CTC CTC AAC CTC GCG ATC TCT GAC CTC TTT TTC CTT CTT
lys ser met thr asp ile tyr leu leu asn leu ala ile cor asp leu phe phe leu leu
301 / 101      331 / 111
ACT GTC CCC TTU TCG CCT CAC TAC TTG CCG CTC CAG TCG GAC TTT GGA AAT ACA ATG TGT
thr val pro phe trp ala his tyr leu ala ala gln trp asp phe gly asn thr met cys
361 / 121      391 / 131
CAA CTC TTG ACA GCG CTC TAT TTT ATA GCG TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC
gln leu leu thr gly leu tyr phe ile gly phe phe ser gly ile phe phe ile ile leu
421 / 141      451 / 151
CTG ACA ATC GAT AGC TAC CTC GCT GTC CTC CAT GCT GTG TTT CCT TTA AAA GCG AGG AGG
leu thr ile asp arg tyr leu ala val val his ala val phe ala leu lys ala arg thr
481 / 161      511 / 171
GTC AAG TTT GCG GTG GTG ACA AGT CTC ATC ACT TCG GTG GTG GCT GTG TTT GCG TTT CTC
val thr phe gly val val thr ser val ile thr trp val val ala val phe ala ser leu
541 / 181      571 / 191
CCA GGA ATC ATC TTT AGC AGA TCT CAA AAA GAA GGT CTT CAT TAC ACC TGC ACC TCT CAT
pro gly ile ile phe thr arg ser gln lys glu gly leu his tyr thr cys ser cor his
601 / 201      631 / 211
TTT CCA TAC AGT CAG TAT CAA TTC TCG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG
phe pro tyr ser gln tyr gln phe trp lys asn phe gln thr leu lyc ile val ile leu
661 / 221      691 / 231
GCG CTG GTC CTC CCG CTG CTT GTC ATG GTC ATC TCG TAC TCG CCA ATC CTA AAA AAT CTC
gly leu val leu pro leu leu val met val ile cys tyr ser gly ile leu lys thr leu
721 / 241      751 / 251
CTT CCG TGT CCA AAT GAG AAG AAG AGG CAC AAG GGT GTG AGC CTT ATC TTC ACC ATC ATG
leu arg cys arg asn glu lys lys arg his arg ala val arg leu ile phe thr ile met
781 / 261      811 / 271
ATT GTT TAT TTT CTC TTC TCG CCG CCC TAC AAC ATT GTC CTT CTC CTC AAG ACC TTC CAG
ile val tyr phe leu phe trp ala pro tyr asn ile val leu leu leu asn thr phe gln
841 / 281      871 / 291
GAA TTC TTT GCG CTC AAT AAT TCG AGT AGC TCT AAC AGC TTS GAC CAA GCT ATC CAG GTG
glu phe phe gly leu asn asn cys ser ser ser asn arg leu asp gln ala met gln val
901 / 301      931 / 311
ACA GAG ACT CTT GCG ATC AGC CAC TCG TAC ATC AAC CCC ATC ATC TAT CCC TTT GTC CCG
thr glu thr leu gly met thr his cys cys ile asn pro ile ile tyr ala phe val gly
961 / 321      991 / 331
GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCG AAA CCG TTC TCG
glu lys phe arg asn tyr leu leu val phe phe gln lys his ile ala lys arg phe cys
1021 / 341      1051 / 351
AAA TCG TGT TCT ATT TTC CAG GAA CAG GCT CCC GAG CCA GCA AGC TCA GTT TAC ACC CGA
lys cys cys ser ile phe gln gln glu ala pro glu arg ala ser ser val tyr thr arg
1081 / 361      1111 / 371
TCC ACT GCG GAG CAG GAA ATA TCT GTC GCG TTG TCA CAC GCA CTC AAG TCG GCT GCT GAC
ser thr gly glu gln glu ile ser val gly leu leu his gly leu lys trp ala gly asp
1141 / 381      1171 / 391
CCA CTC AGA GTT GTC CAC ATG GCT TAG TTT TCA TAC ACA GCG TCG GCT GCG GCG GTG
pro val arg val val his set ala amb phe ser tyr thr ala trp ala gly gly val
1201 / 401      1231 / 411
CCA GAG CTC TTT TTT AAA AGG AAG TTA CTG TTA TAG AGC CTC TAA CAT TCA TCG AT
gly glu val phe phe lys arg lys leu leu leu amb arg val och asp ser ser

```

FIGURE 1B

Figure 1C

SEQ ID NO:3

1 aagaaactct ccccggtgg aacaagatgg attatcaagt gtcaagtcca atctatgaca
61 tcaattatta tacatcggag ccttgccaaa aaatcaatgt gaagcaaate gcagcccgcc
121 tctcgctcc gctctactca ctggtgcca tcttggtt tctgggcaac atgttggtca
181 tctctatcct gataaactgc aaaaggctga agagcatgac tgacatctac ctgctcaacc
241 tggccatctc tgacctgttt ttcttctta ctgtccctt ctgggctcac tatgtgccg
301 cccagtggga ctttggaat acaatgtgtc aactctgac agggctctat ttataggct
361 tcttctctgg aatctcttc atcatcctcc tgacaatcga taggtacctg gctgtctcc
421 atgtgtgtt tgccttaaaa gccaggacgg tcaccttgg ggtggtgaca agtgtgatca
481 ctgggtggt gctgtgttt gcgtctctcc caggaatcat cttaccaga tctcaaaaag
541 aaggcttca ttacacctgc agctctcatt ttccatacag tcagtatcaa ttctggaaga
601 attccagac attaaagata gtcactctgg ggctggctct gccgtgctt gtcagtgtca
661 tctgtactc gggaatccta aaaactctgc ttcggtgtcg aaatgagaag aagaggcaca
721 gggctgtgag gcttatctc accatcatga ttgtttatt tcttctctgg gctccctaca
781 acattgtct tctctgaac acctccagg aattcttgg cctgaataat tgcagtact
841 ctaacaggt ggaccaagct atgcaggtga cagagactct tgggatgacg cactgtctga
901 tcaacccat catctatgcc ttgtcgggg agaagttcag aaactacctc ttagtctct
961 tccaaaagca cattgccaaa cgttctgca aatgctgtt tattttccag caagaggctc
1021 ccgagcgagc aagctcagtt tacacccgat cactgggga gcaggaaata tctgtgggt
1081 tgtgacagg actcaagtgg gctggtgacc cagtacaggt tgtgcacatg gcttagttt
1141 catacacagc ctgggctggg ggtggggtgg gagaggctt tttaaagg aagtactgt
1201 tatagagggt ctaagattca tccat

SEQ ID NO:4

MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL
K3MTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQ
LLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFAS
LPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGIL
KTLRLCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLD
QAMQVTETLGMTHCCINPIYAFVGEKFRNYLLVFFQKHIKRFCCKCSIFQQEAPER
ASSVYTRSTGEQEISVGL

Effects of CCR5 Synthetic Peptides on HIV Env-Mediated Fusion

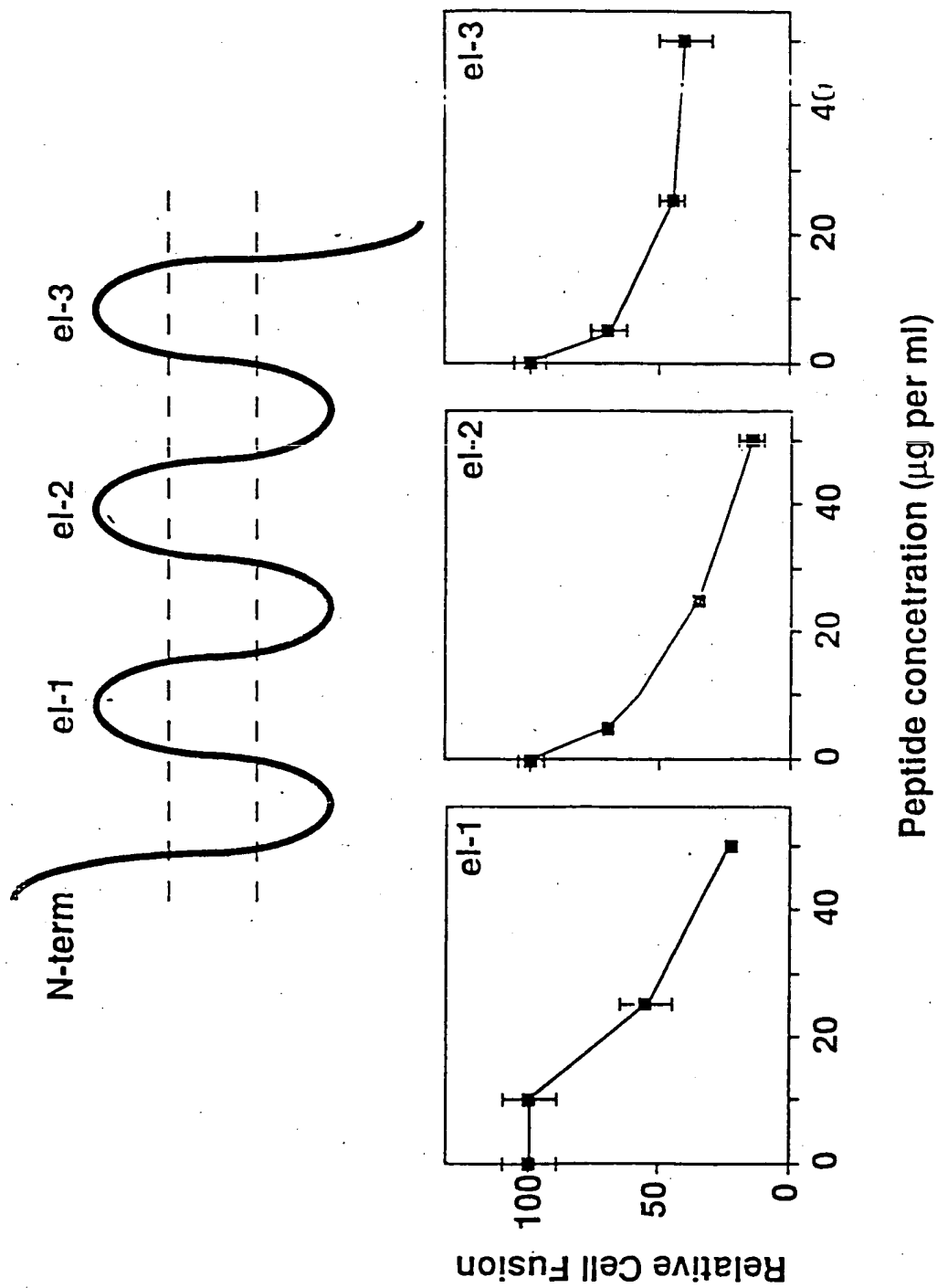


FIGURE 2